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DIPLOID VGS CELLS

↓ POLY (I,C)
↓ CYCLOHEXIMIDE

INDUCED DIPLOID VGS CELLS

↓ (1) LYSIS
↓ (2) EXTRACTION

TOTAL RNA

↓ OLIGO (dT) CELLULOSE
↓ FORMAMIDE-SUCROSE GRADIENT

Ym RNA Xm RNA
Zm RNA FIFm RNA
POLY (A) RNA

↓ REVERSE
↓ TRANSCRIPTASE

Yc DNA Xc DNA
Zc DNA FIFc DNA

DOUBLE STRANDED cDNA

↓ dTTP/TERMINAL
↓ DEOXYNUCLEOTIDYL TRANSFERASE

5' TTT TTT TTT TTT TTT TTT TTT TTT
3' TTT TTT TTT TTT TTT TTT TTT TTT

Pst I AAA Pst I
Amp^R TTT TTT
TET^R

pBR 322-Yc DNA

AAA TTT TTT

pBR 322-Zc DNA

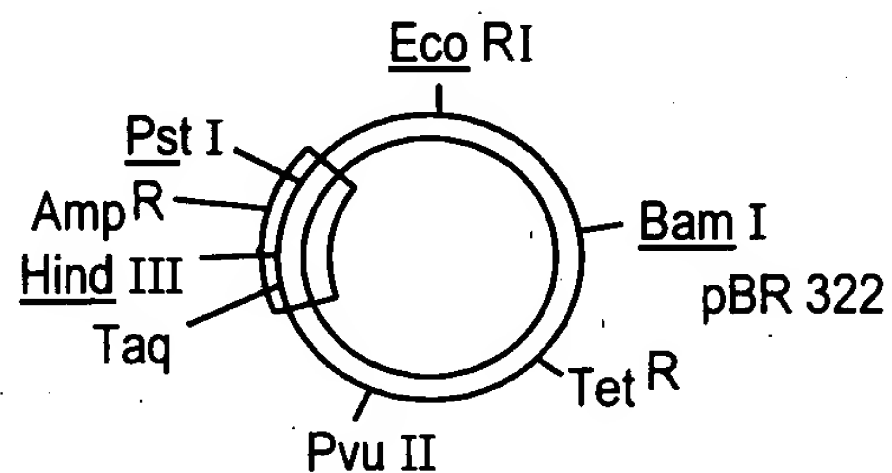
AAA TTT TTT

pBR 322-Xc DNA

AAA TTT TTT

pBR 322-FIFc DNA

FIG. 1



(1) Pst I
(2) dATP/TERMINAL
↓ DEOXYNUCLEOTIDYL
↓ TRANSFERASE

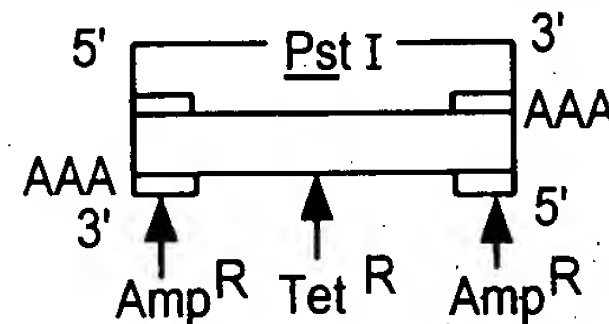
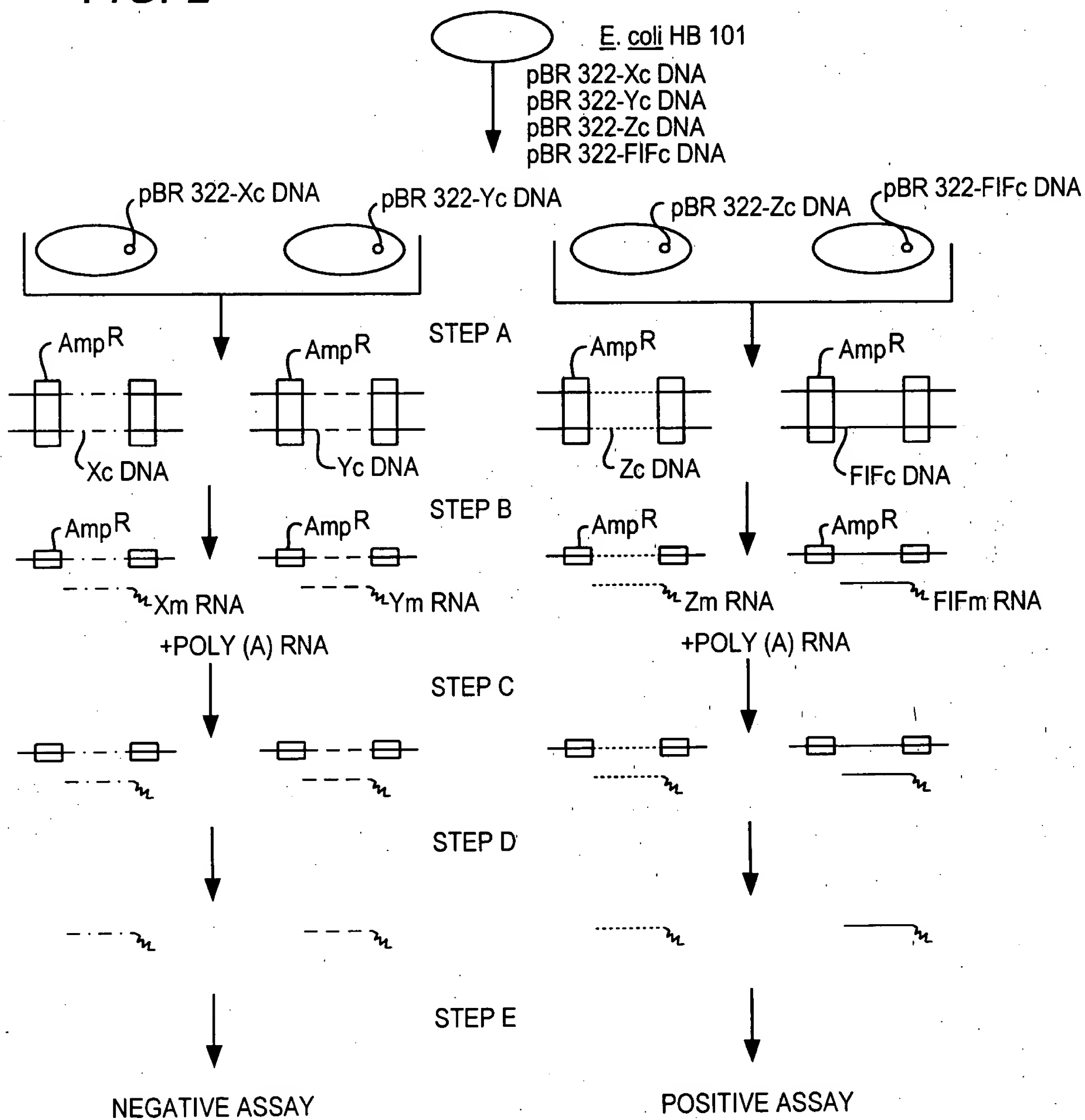


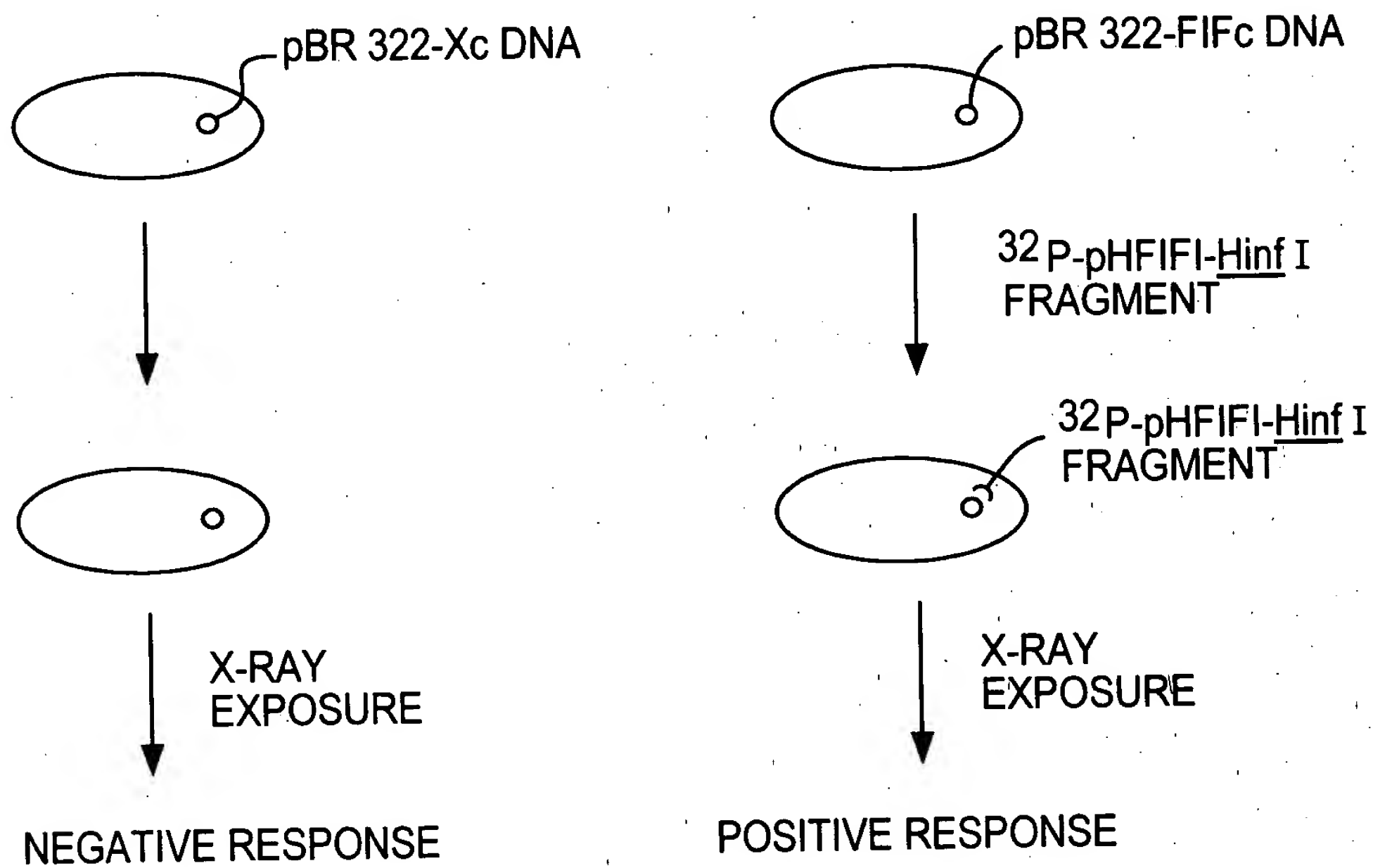
FIG. 2





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FIG. 3





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FIG. 4

-10
MET-THR-ASN-LYS-CYS-LEU-LEU-GLN-ILE-ALA-LEU-LEU-
GCAA CCTTTCGAAG CCTTTCGCTC GGCACAACAG GTAGTAGGCG ACACGTGTCG TGTGTTGAC ATG,ACC,AAC,AAG,TGT,CTC,CTC,CAA,ATT,GCT,CTC,CTG,100

-20
LEU-CYS-PHE-SER-THR-ALA-LEU-SER-MET-SER-TYR-ASN-LEU-GLY-PHE-LEU-GLN-ARG-SER-SER-ASN-PHE-GLN-CYS-GLN-LYS-LEU-LEU-
TTG,TGC,TTT,CTC,ACT,ACA,GCT,CTT,TCC,ATG,AGC,TAC,AAC,TTG,CTT,GGA,TTT,CTA,CAA,AGA,AGC,AGC,AAT,TTT,CAG,TGT,CAG,AAG,CTC,CTG,190

-1 +1
LEU-CYS-PHE-SER-THR-ALA-LEU-SER-MET-SER-TYR-ASN-LEU-GLY-PHE-LEU-GLN-ARG-SER-SER-ASN-PHE-GLN-CYS-GLN-LYS-LEU-LEU-
TTG,TGC,TTT,CTC,ACT,ACA,GCT,CTT,TCC,ATG,AGC,TAC,AAC,TTG,CTT,GGA,TTT,CTA,CAA,AGA,AGC,AGC,AAT,TTT,CAG,TGT,CAG,AAG,CTC,CTG,190

20
TRP-GLN-LEU-ASN-GLY-ARG-LEU-GLU-TYR-CYS-LEU-LYS-ASP-ARG-MET-ASN-PHE-ASP-ILE-PRO-GLU-GLU-ILE-LYS-GLN-LEU-GLN-PHE-GLN-
TGG,CAA,TTG,AAT,GGG,AGG,CTT,GAA,TAC,TGC,CTC,AAG,GAC,AGG,ATG,AAC,TTT,GAC,ATC,CCT,GAG,GAG,ATT,AAG,CAG,CTG,CAG,CTC,CAG,280

30
Lys-GLU-ASP-ALA-ALA-LEU-THR-ILE-TYR-GLU-MET-LEU-GLN-ASN-ILE-PHE-ARG-GLN-ASP-SER-SER-THR-GLY-TRP-ASN-GLU-
AAG,GAG,GAC,GCC,GCA,TTG,ACC,ATC,TAT,GAG,ATG,CTC,CAG,AAC,ATC,TTT,GCT,ATT,TTT,AGA,CAA,GAT,TCA,TCT,AGC,ACT,GGC,TGG,AAT,GAG,370

40
THR-ILE-VAL-GLU-ASN-LEU-ALA-ASN-VAL-TYR-HIS-GLN-ILE-ASN-HIS-LEU-LYS-THR-VAL-LEU-GLU-GLU-LYS-LEU-GLU-LYS-GLU-ASP-PHE-
ACT,ATT,GTT,GAG,AAC,CTC,CTG,GCT,AAT,GTC,TAT,CAT,CAG,ATA,AAC,CAT,CTG,AAG,ACA,GTC,CTG,GAA,GAA,GAA,AAA,GAG,GAT,TTT,460

50
THR-ARG-GLY-LYS-LEU-MET-SER-SER-LEU-HIS-LEU-LYS-ARG-TYR-TYR-GLY-ARG-ILE-LEU-HIS-TYR-LEU-LYS-ALA-LYS-GLU-TYR-SER-HIS-CYS-
ACC,AGG,GGA,AAA,CTC,ATG,AGC,AGT,CTG,CAC,CTG,CAA,AGA,TAT,TAT,GGG,AGG,ATT,CTG,CAT,TAC,CTG,AAG,GCC,AAA,GAG,TAC,AGT,CAC,TGT,550

60
ALA-TRP-THR-ILE-VAL-ARG-VAL-GLU-ILE-LEU-ARG-ASN-PHE-TYR-PHE-ILE-ASN-ARG-LEU-THR-GLY-TYR-LEU-ARG-ASN-
GCC,TGG,ACC,ATA,GTC,AGA,GTG,GAA,ATC,CTA,AGG,AAC,TTT,TAC,TTT,ACA,AGC,CTT,ACA,GGT,TAC,CTC,CGA,AAC,TGA AGATCTCCIA GCCIG643

70
TGCCT CTGGGACIGG ACAATTGCTT CAAGCATTCT TCAACCAGCA GATGCTGTTT AAGTGACTGA TGGCTAATGT ACTGCATATG AAAGGACACT AGAAGATTTT GAAAT 753

80
TTTTA TTAAATTATG AGTTATTTT ATTTATTAA ATTTATTTT GGAAATAAATTATTTTGG TGCAAAGTC AAAAAAAA, ...

OIPE
 JUL 14 2003
 PATENT & TRADEMARK OFFICE

Applicant: Walter...
 Filed: May 25, 1995
 Application No.: 08/452,658
 Agent: Bhavana Joneja (Reg. No. 47,689) Express Mail EV132183926US
 For: DNA SEQUENCES, RECOMBINANT DNA MOLECULES AND PROCESS FOR PRODUCING HUMAN FIBROBLAST INTERFERON-LIKE POLYPEPTIDES

Docket No. B8/B8 CIP DIV4
 Conf. No. 5499

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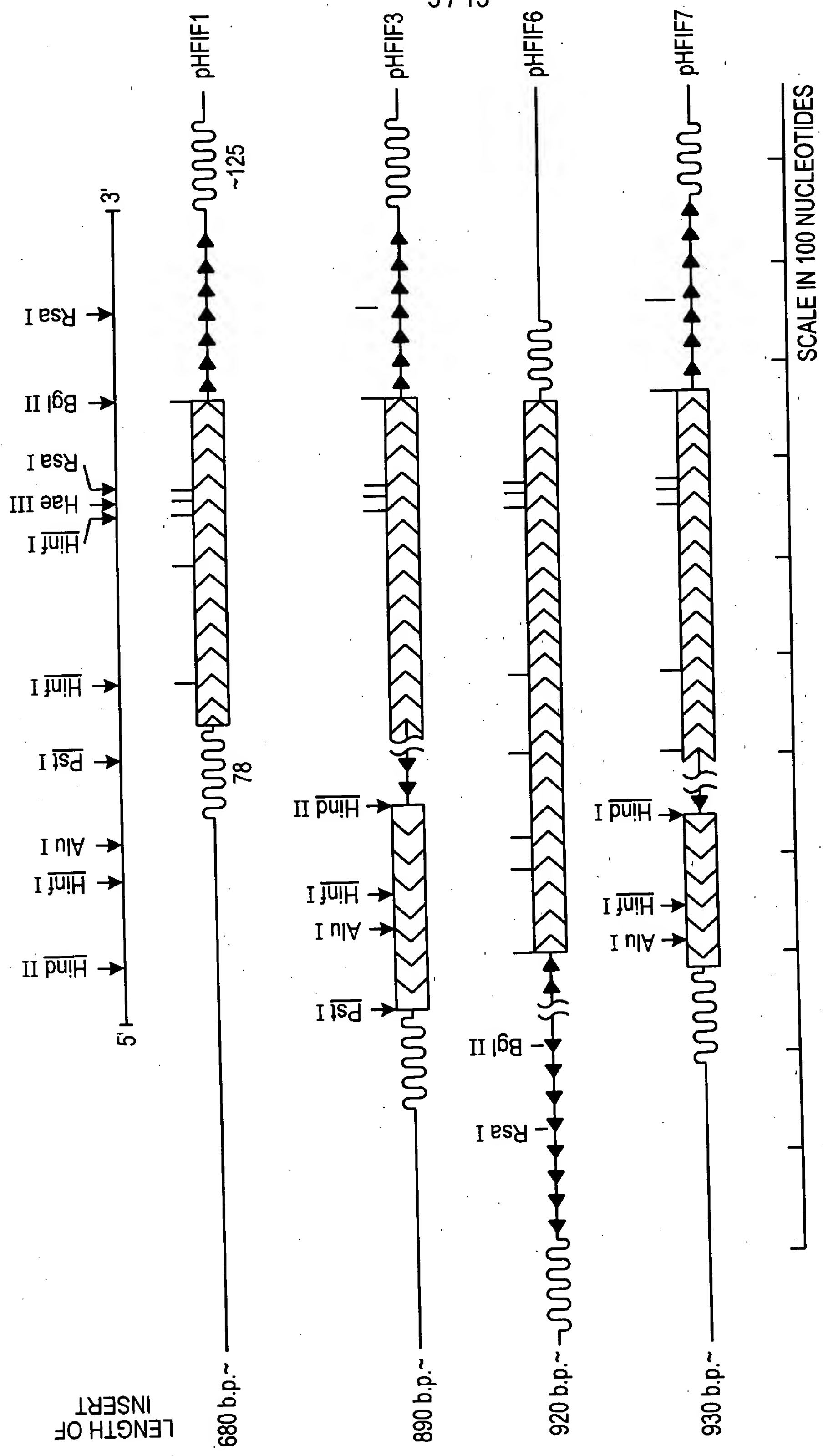


FIG. 5

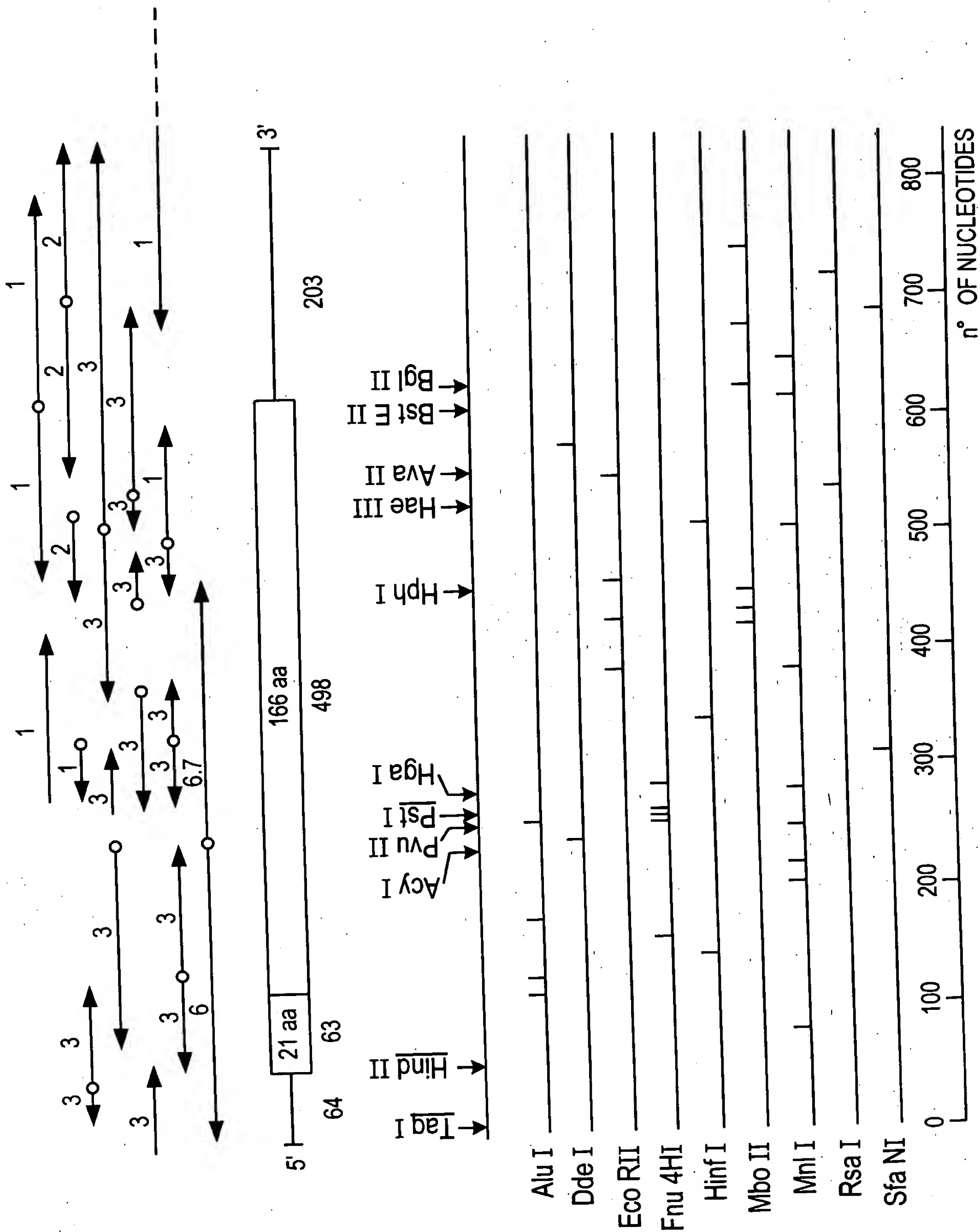


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AMINO ACID COMPOSITION OF HUMAN FIBROBLAST INTERFERON

AMINO ACID	COMPOSITION		
	FROM DIRECT ANALYSIS BY TAN ET AL.	FROM DIRECT ANALYSIS BY KNIGHT ET AL.	DEDUCED FROM NUCLEOTIDE SEQUENCE
ASP	} 20.6	18.9	5
ASN			12
THR	8.0	6.8	7
SER	11.7	10.5	9
GLU	} 27.5	27.0	13
GLN			11
PRO	4.4	2.7	1
GLY	5.4	7.8	6
ALA	9.3	10.0	6
CYS	N.D.	1.7	3
VAL	7.9	6.0	5
MET	trace	2.9	4
ILE	10.0	9.0	11
LEU	26.9	20.4	24
TYR	3.2	7.5	10
PHE	7.7	9.4	9
HIS	4.6	4.9	5
LYS	12.3	11.6	11
ARG	8.6	10.9	11
TRP	0.0	1.0	3
TOTAL	168	169	166

FIG. 6



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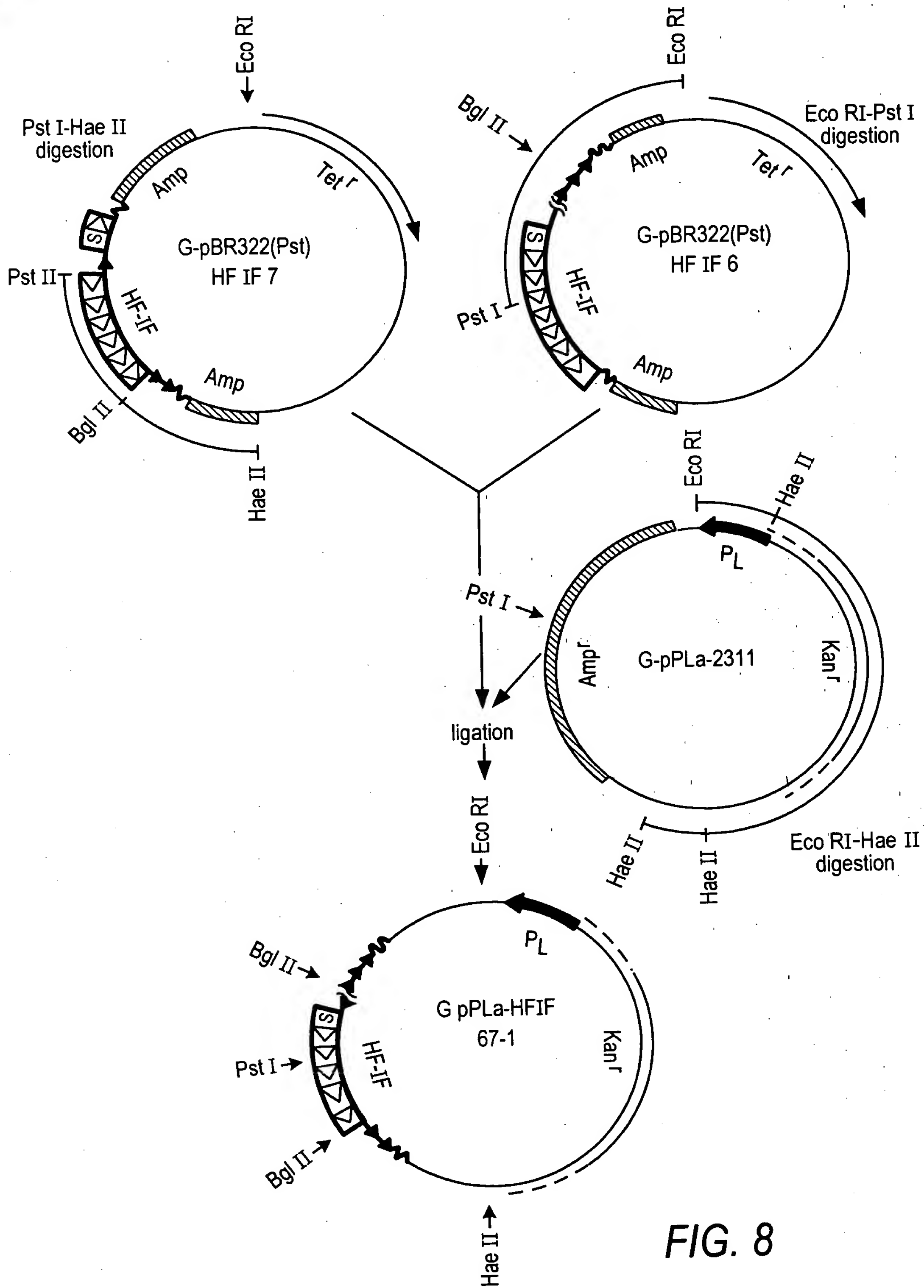


FIG. 8



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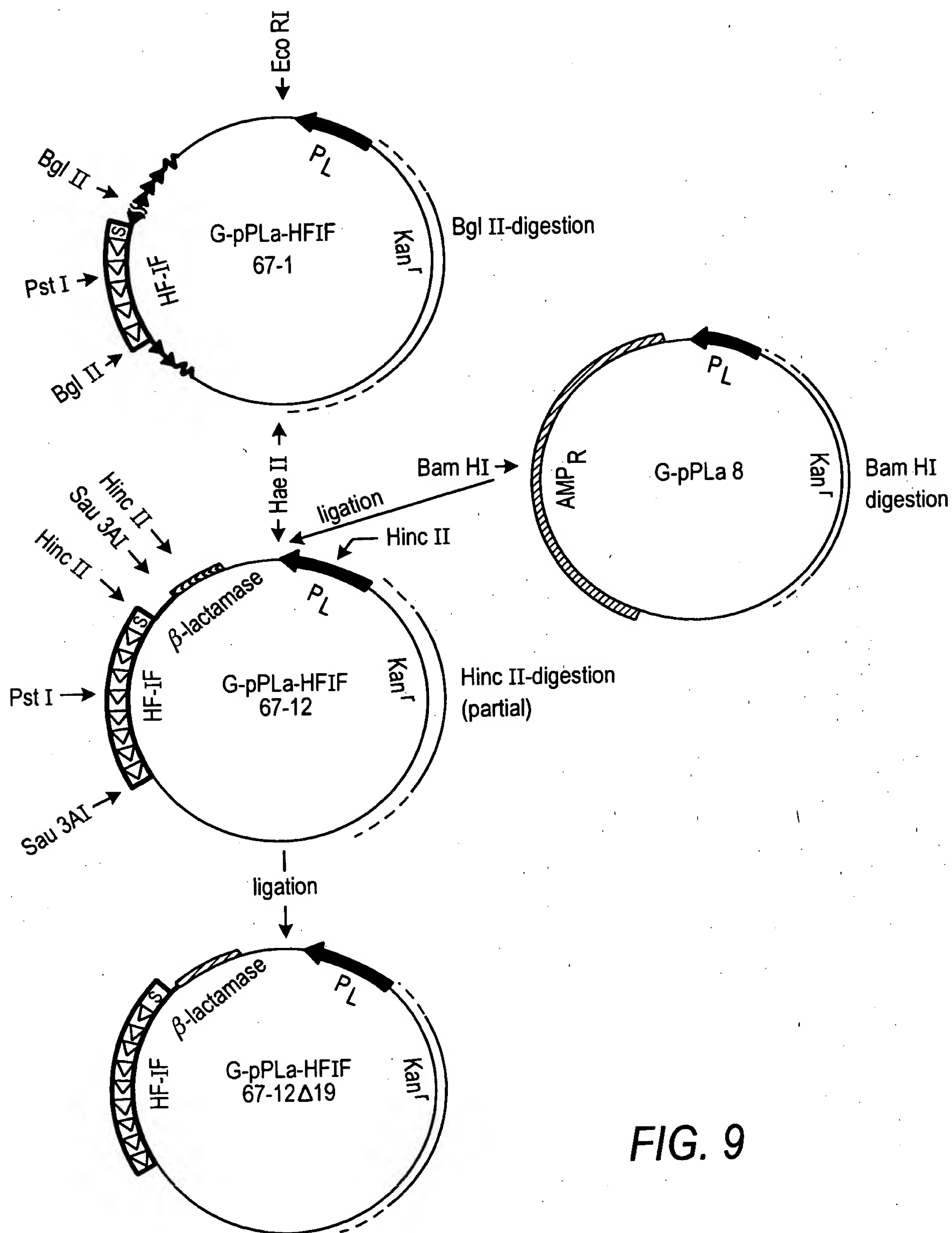


FIG. 9

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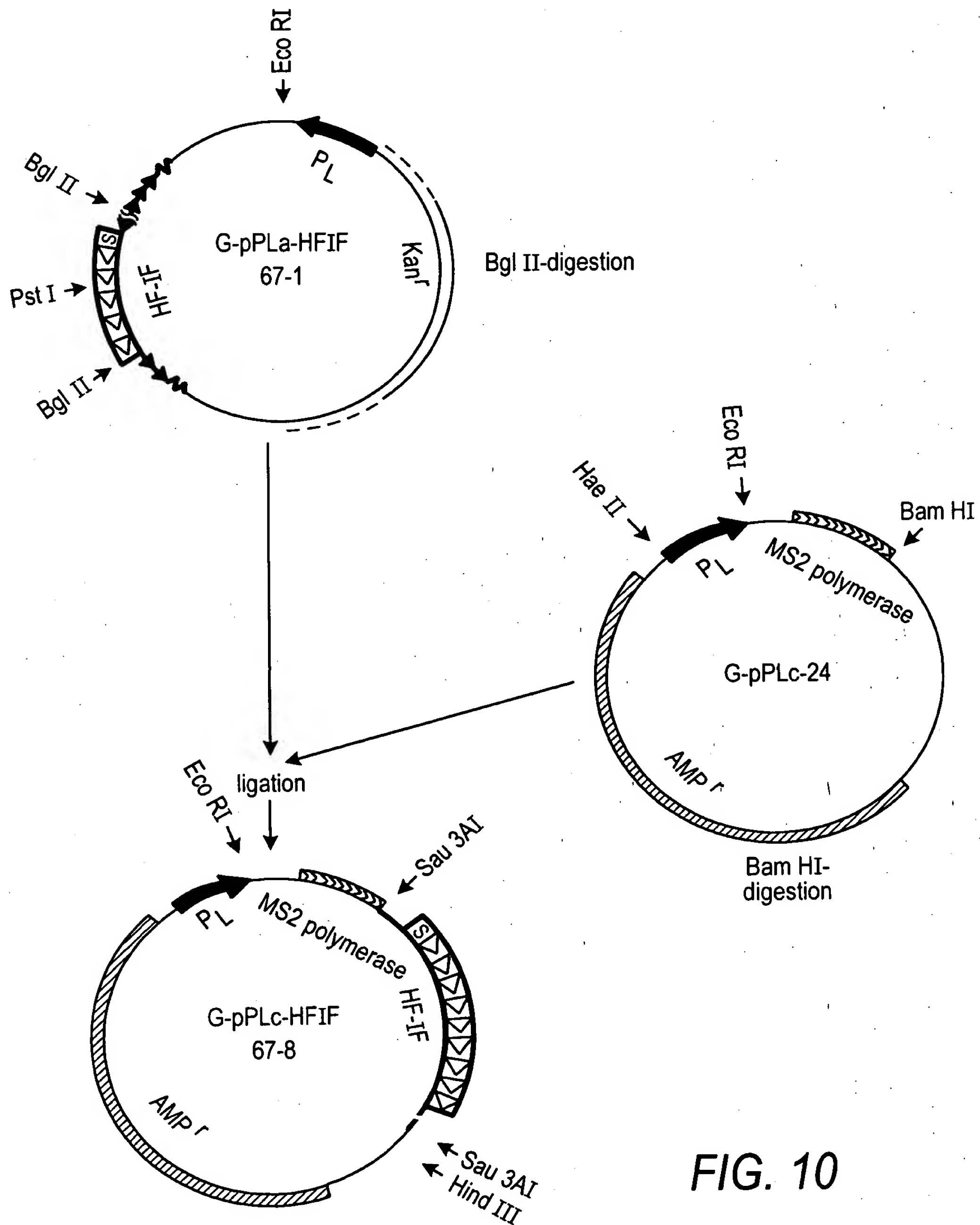


FIG. 10

FIG. 11

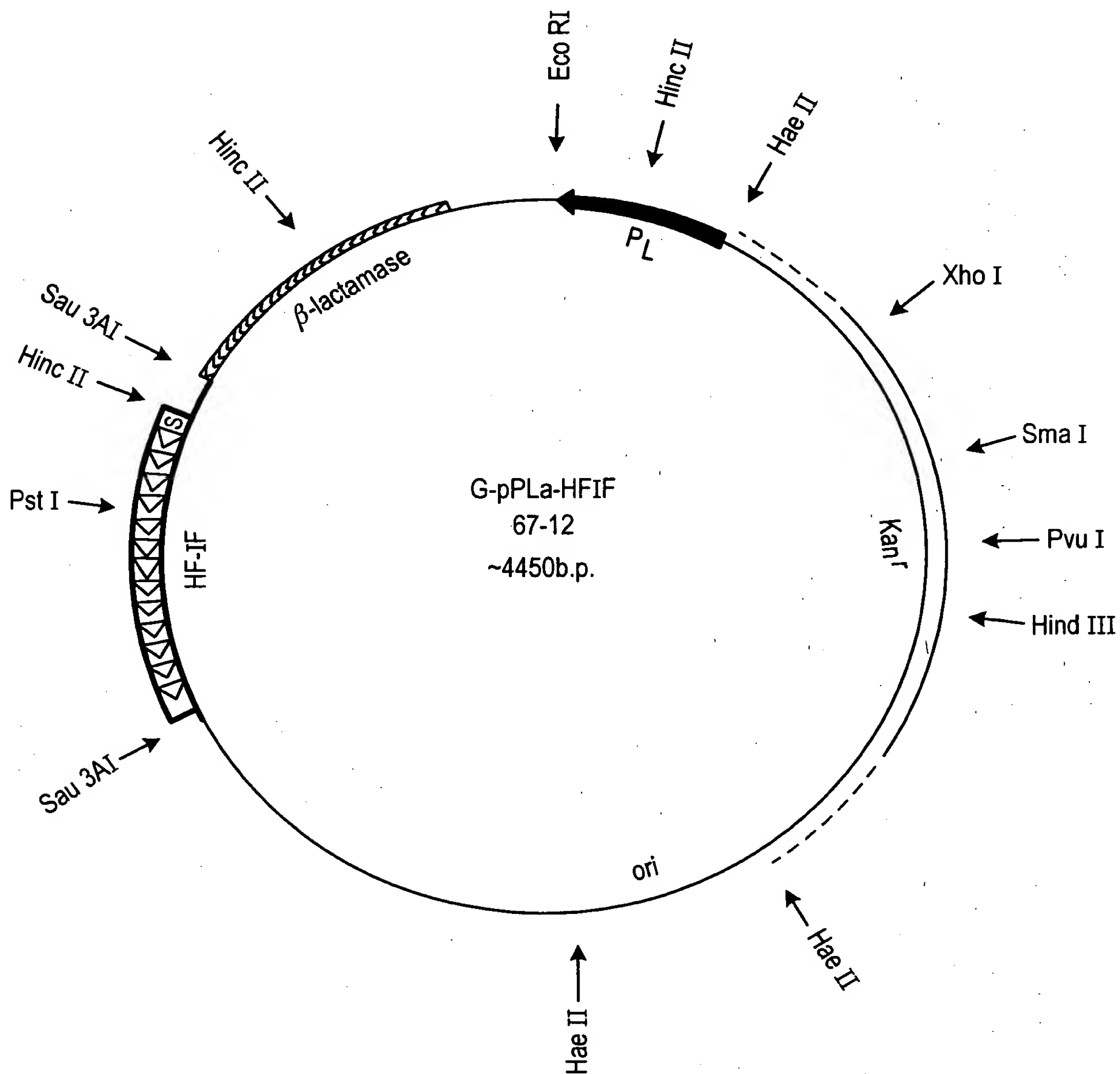




FIG. 12

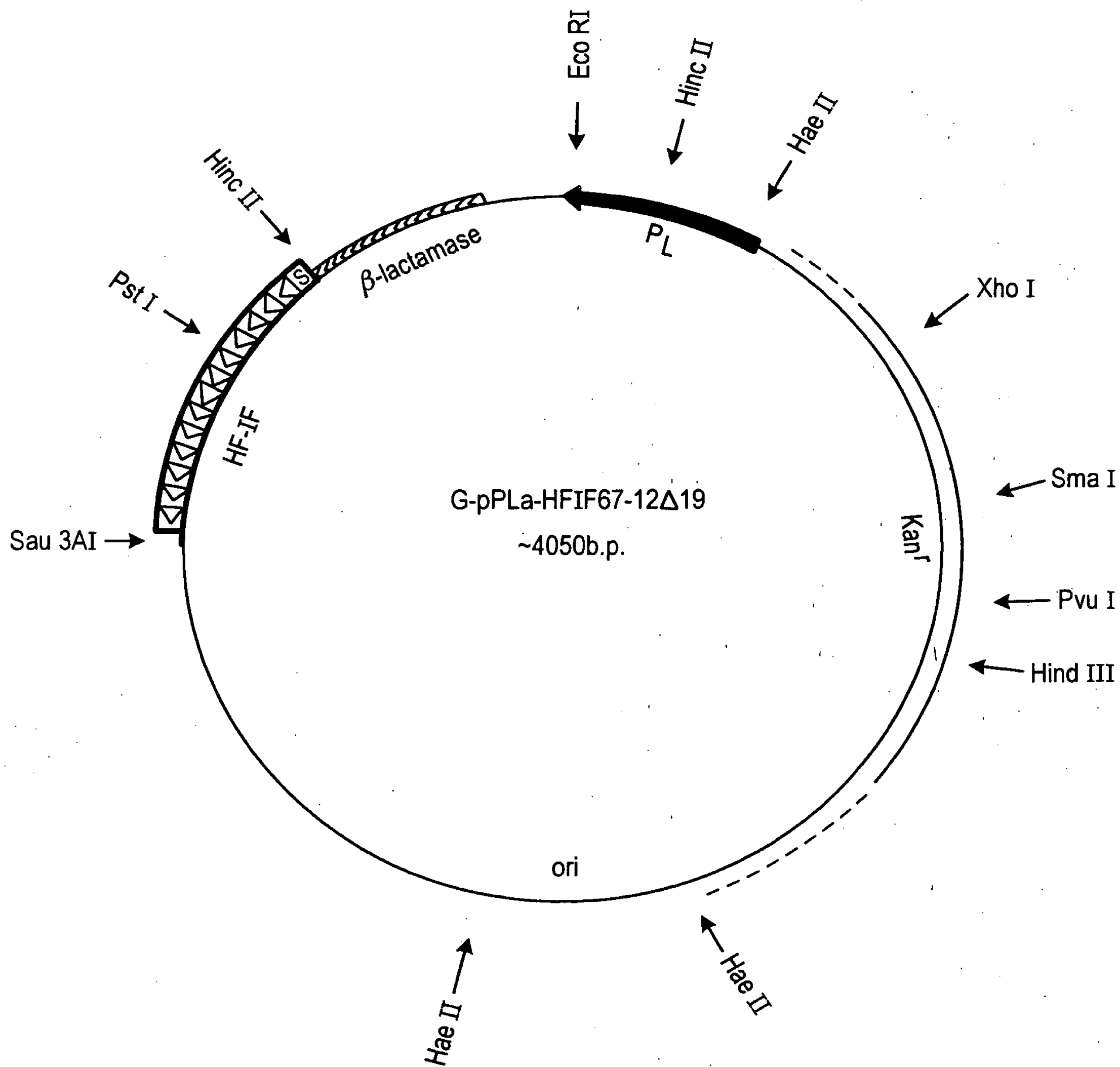


FIG. 13

